

FIG. 1

BLASTP - query = 147_TR1; Hit = swiss|O15393|TMS2_HUMAN

This hit is scoring at : 3e-66 (expectation value)

Alignment length (overlap) : 370

Identities : 38 %

Scoring matrix : BLOSUM62 (used to infer consensus pattern)

Database searched : nrdb

Q: 36 CDGVVDCKLKSDELGCVRFDWKSLKIIYSGSSHQWLPICSSNWNDSEKTCQQLGFES
CDGV .C. .DE CVR. . . :L::YS.....W P:C...WN::Y....C::G:::
H: 133 CDGVSHCPGGEDENRCVRLYGPNFILQMYSSQRKSWHPVCQDDWNNENYGRAACRDMGYKN

AHRTTEVAHRDFANSFSILRYNST-----IQESLHRSE-CPSQRYISLQCSHCGLR---A
. ::: . D :.S S:::N:: I...L::S: C.S:::SL:C CG:. :
NFYSSQGIVDD-SGSTSFMKLNTSAGNVDIYKKLYHSDACSSKAVVSLRCLACGVNLNSS

MTGRIVGGALASDSKWPQVSLHFGTTHICGGTLIDAQWVLTAAHCFFVTREKVLEG---
...RIVGG. A ...WPWQVSLH. ..H:CGG::I...W::TAHC. EK L..
RQSRIVGGESALPGAWPQVSLHVQNVHVCGGSIIITPEWIVTAAHCV----EKPLNNPWH

TRYPSIN_HIS

WKVYAGTSNLHQLPEAAS--IAEIIINSNYTDEEDDYDIALMRLSKPLTLSG--EGICTP
W...AG. . . : .A. ::::I :.NY.....: DIALM:L.KPLT... : :C.P
WTAFAGILRQSFMYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLP

RSPAPQPQHPLQPSHLASVNSYPGPKASADKTSPFLREVQVNLIDFKKCDNYLVYDSYL
. P LQP..L . :::: G.....KTS..L...:V LI: ::CN. .VYD::
N-----PGMMLQPEQL-CWISGW-GATEEKGKTSEVLNAKVLLIETQRCNSRYVYDNLII

TPRMMCAGDLRGGRDSCQGDSSGGPLVCEQNNRWYLAGVTSWGTGCGQRNKPVGVTYTKVTEV
TP.M:CAG L:G. DSCQGDSSGGPLV...NN W:L.G TSWG:GC...:PGVY .V. .
TPAMICAGFLQGNVDSCQGDSSGGPLVTSNNNIWWLIGDTSWGSQCAKAYRPGVYGNVMVF

TRYPSIN_SER

LPWIYSKMEA 389
..WIY.:M:A
TDWIYRQMK 490

BLOCKS

FIG. 2

Prosite search results

PS00134	187->193	TRYPSIN_HIS	PDOC00124
PS00135	334->346	TRYPSIN_SER	PDOC00124

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FIG. 3

BLOCKS search results

AC# Score	Description	Strength	
BL00495N AA#	Apple domain proteins. 325 AGdlrGGrDsCqGDSGGPLVCeqNnRWyLaGvTSW (SEQ ID NO:15)	1945	1582
BL01253G AA#	Type I fibronectin domain proteins. 332 rDsCQGDSGGPLVC (SEQ ID NO:16)	1641	1548
BL00134A AA#	Serine proteases, trypsin family, histidine p 1500 175 CGGTLIDaQWVLTAHC (SEQ ID NO:17)	1524	
BL00021D AA#	Kringle domain proteins. 341 GPLVCEQNNRWYLaGVTSWGtGCGQRNKPVGVTevLPWI (SEQ ID NO:18)	1556	1510
BL01253H AA#	Type I fibronectin domain proteins. 351 wYLaGvtSWGtGCGQRNKPVGVTevLpWIysk (SEQ ID NO:19)	1765	1508
BL00021B AA#	Kringle domain proteins. 175 CGGTLIDaQWVLTAHCF (SEQ ID NO:120)	1547	1507
BL00495O AA#	Apple domain proteins. 360 GtGCGQRnkPGVYTKVtEvlpWIysKmeA (SEQ ID NO:121)	1756	1383
BL00134B AA#	Serine proteases, trypsin family, histidine p 1289 333 DSCQGDSGGPLVCEqNNRWYLAGV (SEQ ID NO:122)	1299	
BL01209 AA#	LDL-receptor class A (LDLRA) domain proteins. 35 CDGVVDCKlKSDE (SEQ ID NO:123)	1413	1274
BL01253F AA#	Type I fibronectin domain proteins. 288 AdktSpFLREvQVnLidfkKCndylVYdSylTPrMmCAG (SEQ ID NO:124)	1693	1270
BL00495L AA#	Apple domain proteins. 209 tSnlhqlpeaaSIaEIIInsNYtdeEddYDIALmrLskP (SEQ ID NO:125)	1947	1263
BL00134C AA#	Serine proteases, trypsin family, histidine p 1245 369 PGVYTKVTEVLPWI (SEQ ID NO:126)	1254	
BL01253D AA#	Type I fibronectin domain proteins. 175 CGGtLIdaqWVLTA (SEQ ID NO:127)	1398	1217

FIG. 4

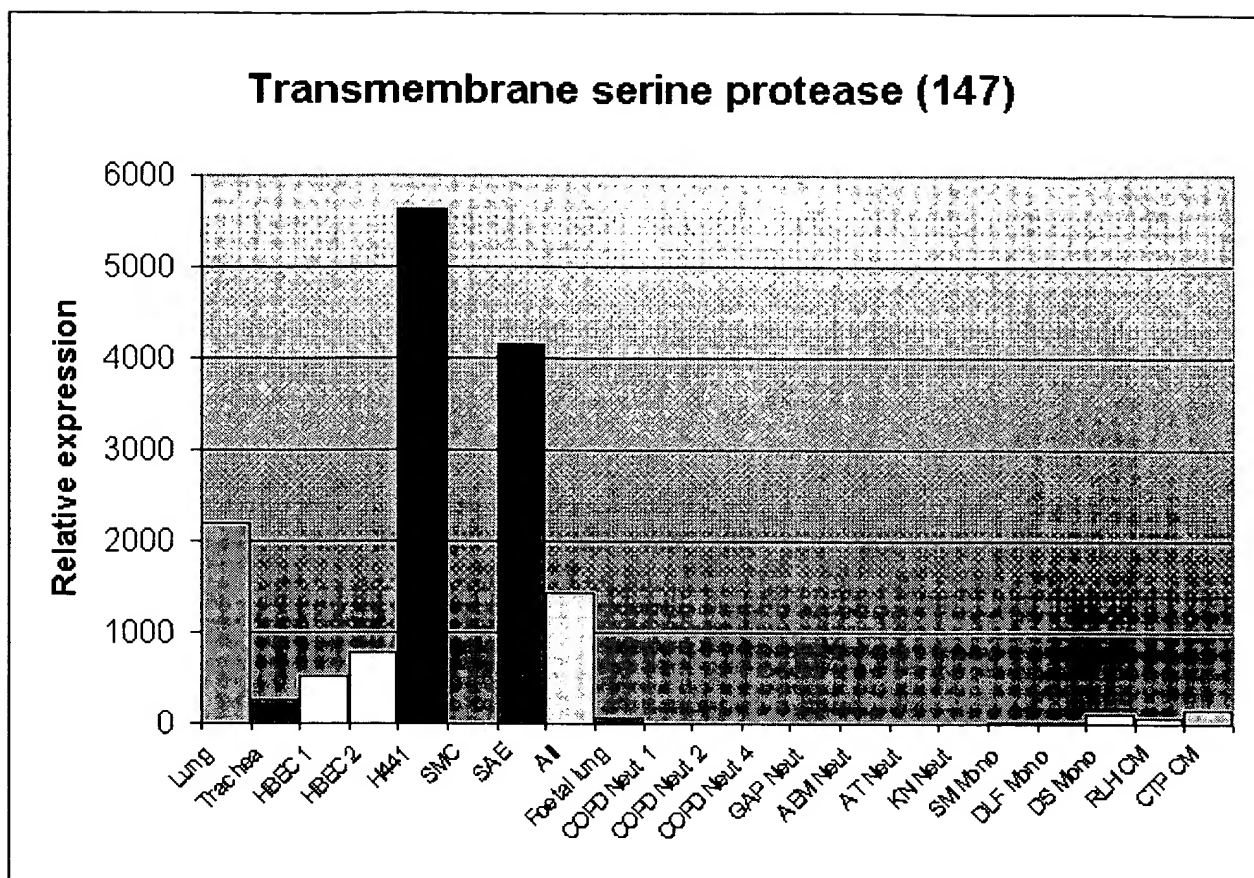
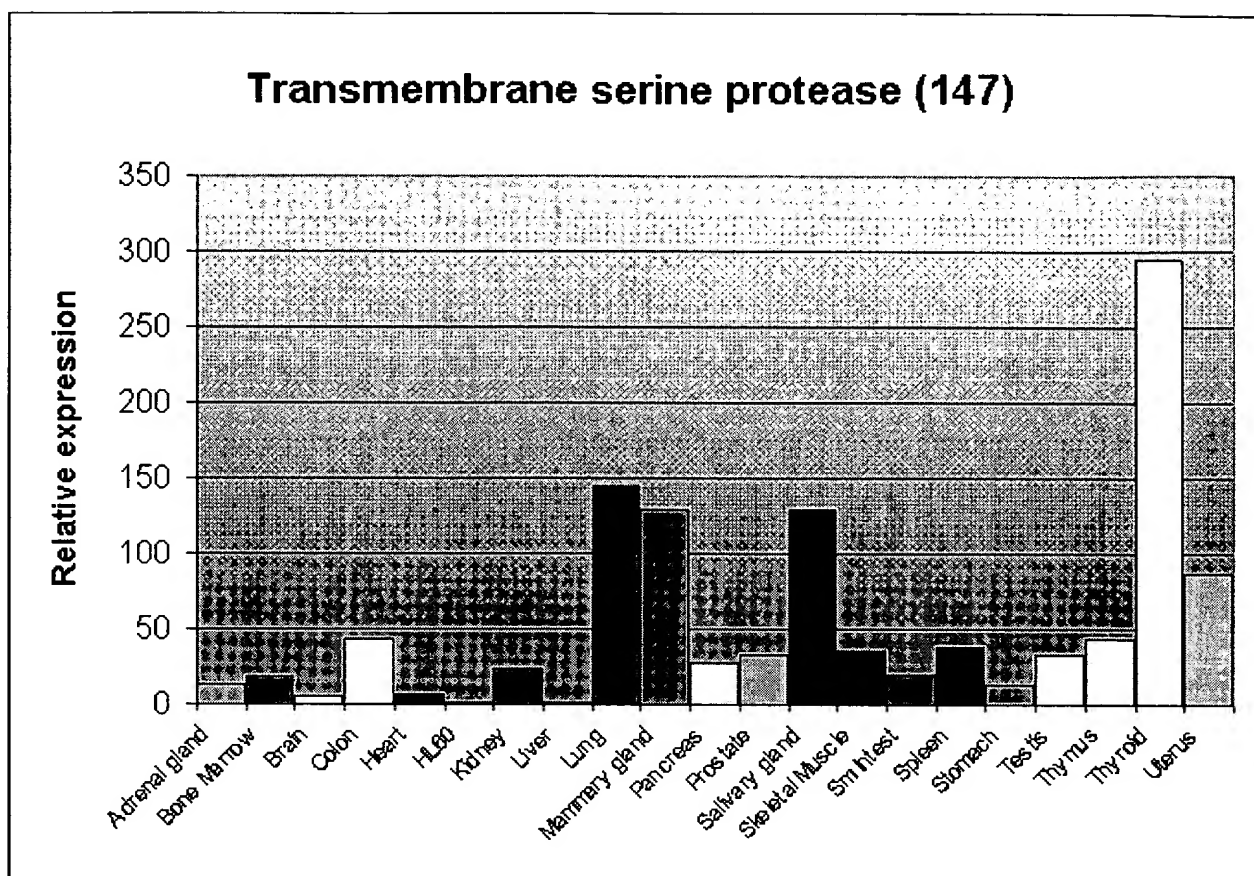
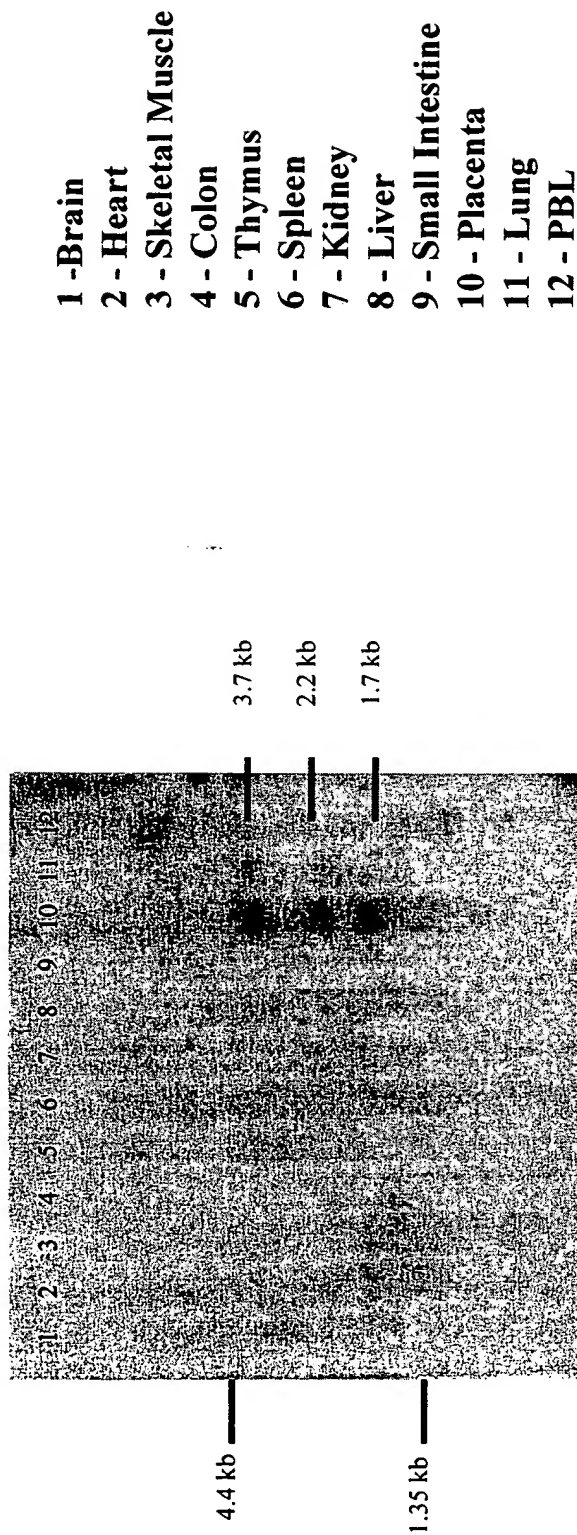


FIG. 5



LBRI - 147 - Transmembrane serine protease



16 hour exposure - Maximum Intensity 2,000

LBRI 147

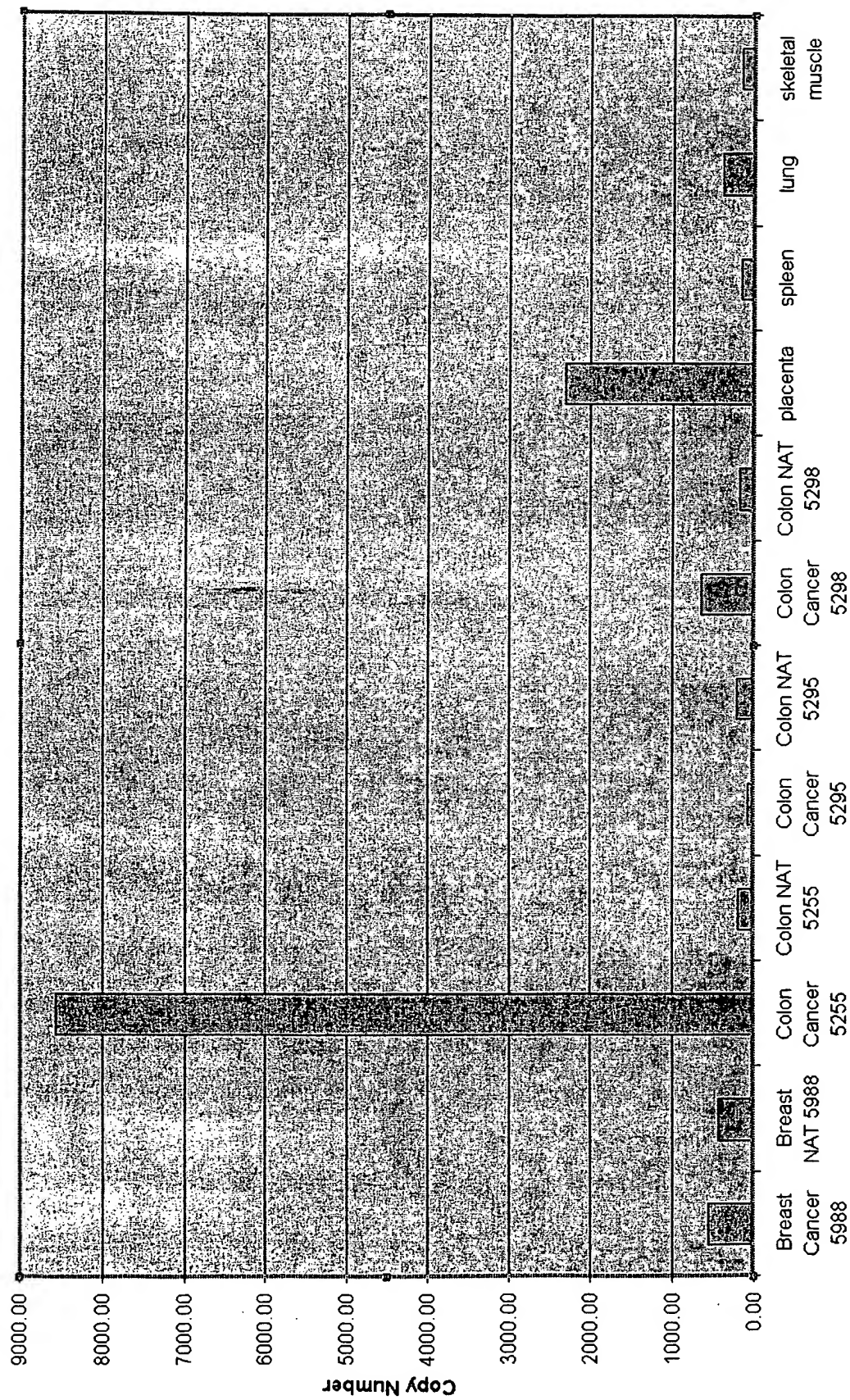
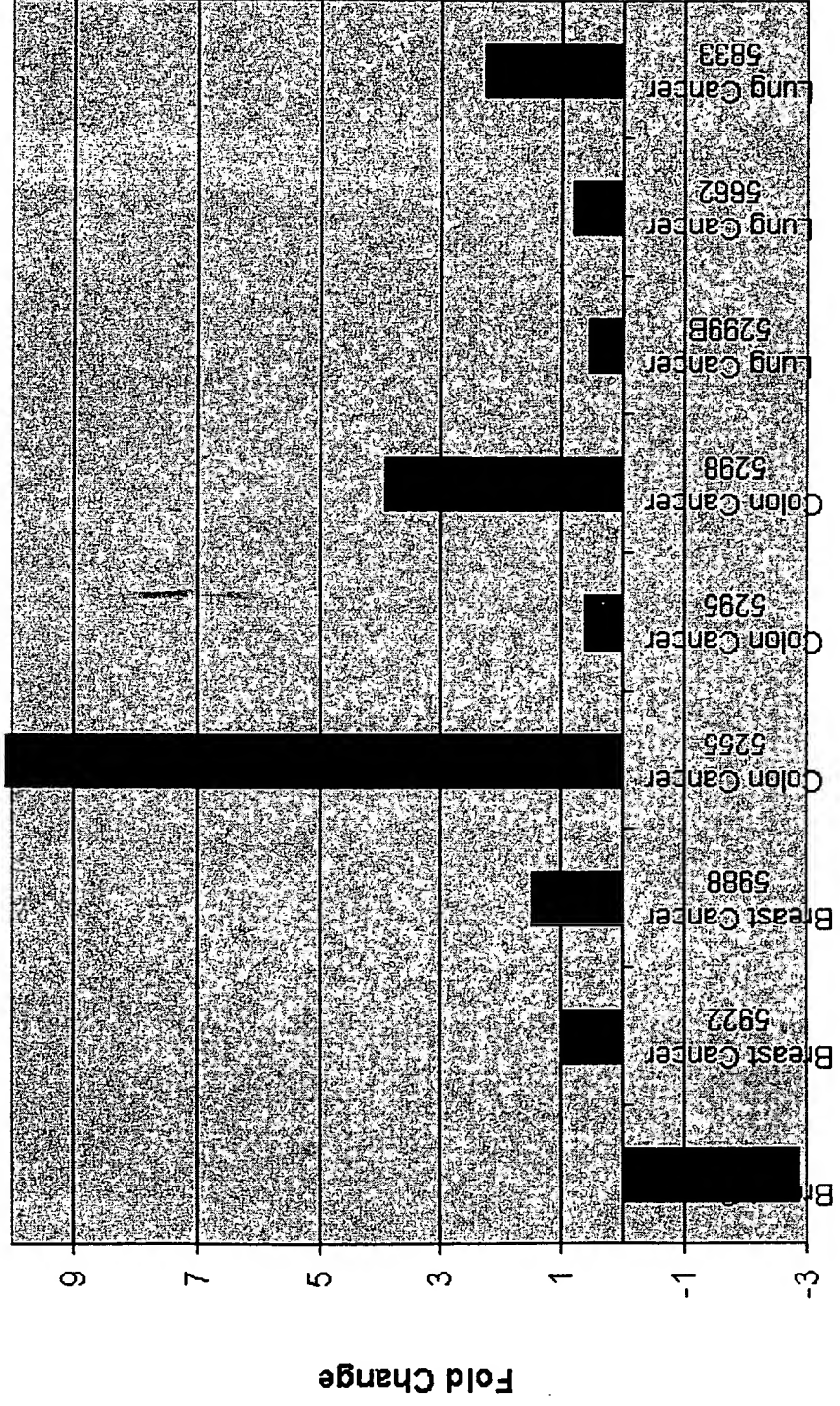


FIG. 7

LBRI 147 - Fold change

74.



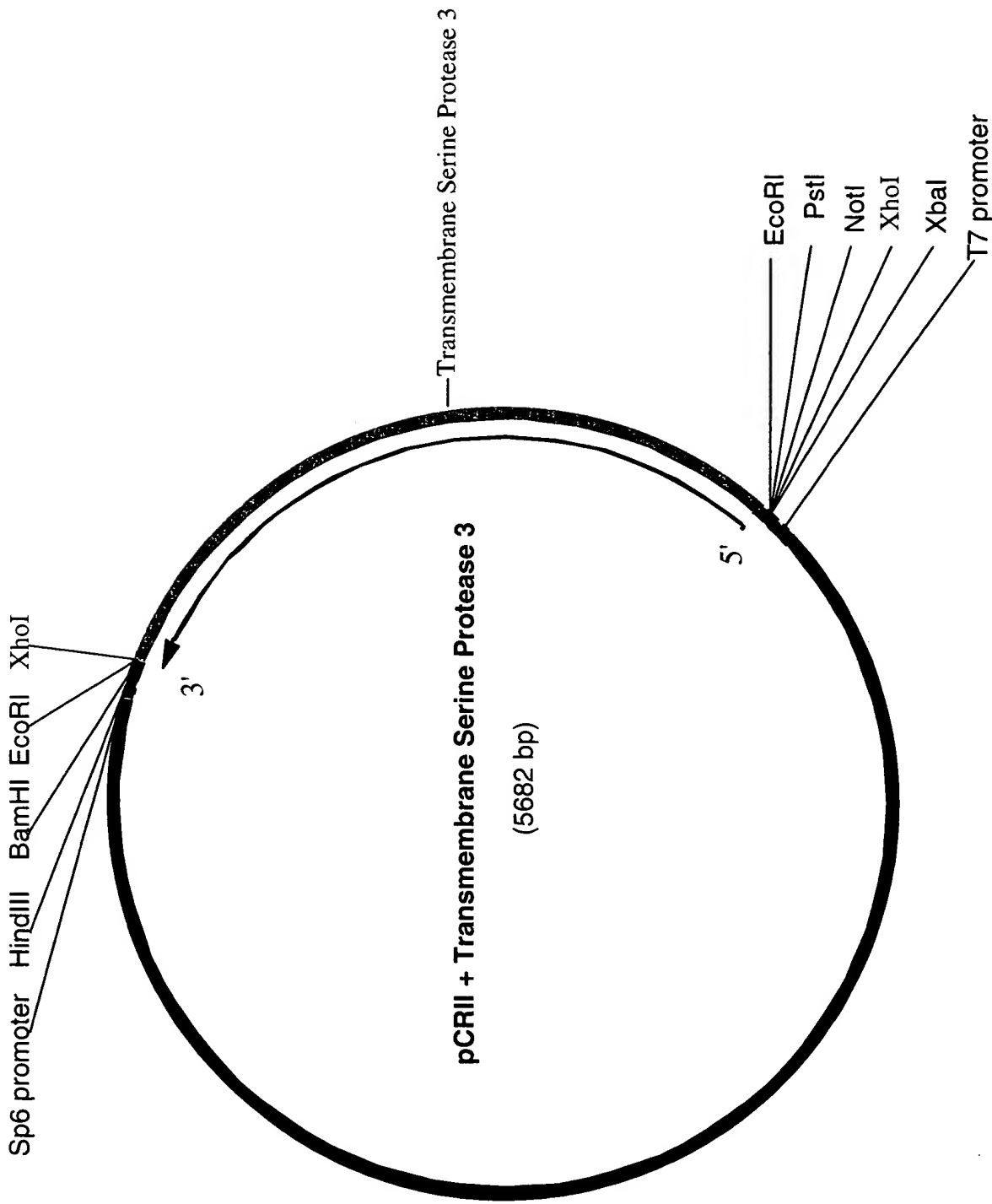


Fig. 9